
Northstar enables automatic classification of known and novel cell types from tumor samples.

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Authors: Fabio Zanini, Bojk A Berghuis, Robert C Jones, Benedetta Nicolis di Robilant, Rachel Yuan Nong, Jeffrey A Norton, Michael F Clarke, Stephen R Quake

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Public Summary:

Scientific Abstract:

Single cell transcriptomics is revolutionising our understanding of tissue and disease heterogeneity, yet cell type identification remains a partially manual task. Published algorithms for automatic cell annotation are limited to known cell types and fail to capture novel populations, especially cancer cells. We developed northstar, a computational approach to classify thousands of cells based on published data within seconds while simultaneously identifying and highlighting new cell states such as malignancies. We tested northstar on data from glioblastoma, melanoma, and seven different healthy tissues and obtained high accuracy and robustness. We collected eleven pancreatic tumors and identified three shared and five private neoplastic cell populations, offering insight into the origins of neuroendocrine and exocrine tumors. Northstar is a useful tool to assign known and novel cell type and states in the age of cell atlases.

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